Listing of Claims

1. (Currently Amended) A method for analyzing the transcriptome of a tissue section comprising analyzing two or more molecular species present in the tissue section while maintaining the 2-dimensional architecture of the molecules within the tissue section, wherein said method comprises:

treating the tissue section with an External Movement Inhibitor device having multiple discrete partitions, wherein the multiple discrete partitions comprise at least one of a plurality of grids or a plurality of wells,

sequestering ~~whereby each grid or well sequesters~~ molecules corresponding to a specific region or cell type of the tissue section in an aqueous solution contained within at least one of the plurality of grids or plurality of wells, thereby preserving the 2-dimensional architecture of ~~the~~ these molecules relative to other molecules present within the tissue section while simultaneously allowing molecule manipulation in the aqueous solution, and

determining the location(s) in the tissue section in which said two or more molecular species are present.

2. (Previously Presented) The method of claim 1, wherein said tissue section is obtained from a mammal.

3. (Original) The method of claim 2, wherein said mammal is a human.

4. (Canceled)

5. (Previously Presented) The method of claim 1, wherein said tissue section is from a biopsy.

6. (Original) The method of claim 1, wherein said molecular species are nucleic acid molecules.

7. (Previously Presented) The method of claim 6, wherein said method additionally comprises incubating the sequestered molecules under conditions sufficient to permit the manipulation of one or more preselected nucleic acid molecules if present in at least one of the plurality of grids or the plurality of wells, while preserving the 2-dimensional architecture of said molecules relative to other molecules of said tissue section.

8 (Withdrawn) The method of claim 7, wherein said method additionally comprises transferring said manipulated nucleic acid species to two or more membranes, said membranes being differentially treated to enable the determination of the location(s) of manipulated nucleic acid species.

9. (Original) The method of claim 7, wherein one or more of said preselected nucleic acid molecule(s) are diagnostic of a disease state.

10. (Original) The method of claim 7, wherein said manipulation is selected from the group consisting of nucleic acid amplification, reverse transcription, labeling, cloning, and the assaying of a biomolecule.

11. (Previously Presented) The method of claim 7, wherein said method comprises incubating the sequestered molecules in the plurality of grids or the plurality of wells under conditions sufficient to permit the manipulation of said one or more preselected nucleic acid molecules.

12. (Original) The method of claim 11, wherein one or more of said preselected nucleic acid molecule(s) are diagnostic of a disease state.

13. (Original) The method of claim 11, wherein said manipulation is selected from the group consisting of nucleic acid amplification, reverse transcription, labeling, cloning, and the assaying of a biomolecule.

14 - 21. (Canceled)

22. (Withdrawn) The method of claim 1, wherein said molecular species are protein molecules.

23. (Withdrawn) The method of claim 22, wherein said cellular sample is an extract of a cell, and said 2-dimensional array is a gel or membrane that arrays said molecules of said extract.

24. (Withdrawn) The method of claim 22, wherein one or more of said protein molecule(s) are diagnostic of a disease state.